



SEQUENCE LISTING

<110> al.

<120> Screens and Assays for Agents Useful in Controlling  
Parasitic Nematodes

<130> 2002630-0012

<140> 10/051,644

<141> 2002-01-18

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 425

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Amino Acid  
Sequence

<400> 1

Met Ala Val Leu Ala Val Val Leu Leu Leu Ala Cys Leu Glu Arg Ala  
1 5 10 15

Val Ala Gln Thr Phe Gly Cys Ser Asn Thr Lys Ile Asn Asp Gln Ala  
20 25 30

Arg Lys Met Phe Tyr Asp Ala His Asn Asp Ala Arg Arg Ser Met Ala  
35 40 45

Lys Gly Leu Glu Pro Asn Lys Cys Gly Leu Leu Ser Gly Gly Lys Asn  
50 55 60

Val Tyr Glu Leu Asn Trp Asp Cys Glu Met Glu Ala Lys Ala Gln Glu  
65 70 75 80

Trp Ala Asp Gly Cys Pro Ser Ser Phe Gln Thr Phe Asp Pro Thr Trp  
85 90 95

Gly Gln Asn Tyr Ala Thr Tyr Met Gly Ser Ile Ala Asp Pro Leu Pro  
100 105 110

Tyr Ala Ser Met Ala Val Asn Gly Trp Trp Ser Glu Ile Arg Thr Val

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115

120

125

Gly Leu Thr Asp Pro Asp Asn Lys Tyr Thr Asn Ser Ala Met Phe Arg  
130 135 140

Phe Ala Asn Met Ala Asn Gly Lys Ala Ser Ala Phe Gly Cys Ala Tyr  
145 150 155 160

Ala Leu Cys Ala Gly Lys Leu Ser Ile Asn Cys Ile Tyr Asn Lys Ile  
165 170 175

Gly Tyr Met Thr Asn Ala Ile Ile Tyr Glu Lys Gly Asp Ala Cys Thr  
180 185 190

Ser Asp Ala Glu Cys Thr Thr Tyr Ser Asp Ser Gln Cys Lys Asn Gly  
195 200 205

Leu Cys Tyr Lys Ala Pro Gln Ala Pro Val Val Glu Thr Phe Thr Met  
210 215 220

Cys Pro Ser Val Thr Asp Gln Ser Asp Gln Ala Arg Gln Asn Phe Leu  
225 230 235 240

Asp Thr His Asn Lys Leu Arg Thr Ser Leu Ala Lys Gly Leu Glu Ala  
245 250 255

Asp Gly Ile Ala Ala Gly Ala Phe Ala Pro Met Ala Lys Gln Met Pro  
260 265 270

Lys Leu Val Lys Tyr Ser Cys Thr Val Glu Ala Asn Ala Arg Thr Trp  
275 280 285

Ala Lys Gly Cys Leu Tyr Gln His Ser Thr Ser Ala Gln Arg Pro Gly  
290 295 300

Leu Gly Glu Asn Leu Tyr Met Ile Ser Ile Asn Asn Met Pro Lys Ile  
305 310 315 320

Gln Thr Ala Glu Asp Ser Ser Lys Ala Trp Trp Ser Glu Leu Lys Asp  
325 330 335

Phe Gly Val Gly Ser Asp Asn Ile Leu Thr Gln Ala Val Phe Asp Arg  
340 345 350

Gly Val Gly His Tyr Thr Gln Met Ala Trp Glu Gly Thr Thr Glu Ile  
355 360 365

Gly Cys Phe Val Glu Asn Cys Pro Thr Phe Thr Tyr Ser Val Cys Gln

370

375

380

Tyr Gly Pro Ala Gly Asn Tyr Met Asn Gln Leu Ile Tyr Thr Lys Gly  
385 390 395 400

Ser Pro Cys Thr Ala Asp Ala Asp Cys Pro Gly Thr Gln Thr Cys Ser  
405 410 415

Val Ala Glu Ala Leu Cys Val Ile Pro  
420 425

<210> 2  
<211> 1341  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:cDNA Nucleotide  
Sequence

<400> 2  
atggcggtat tagcagtgg actacttcta gcatgcctgg agagagcggt tgcacagacg 60  
ttcggctgct ctaacaccaa gatcaatgac caggctcgta agatgttcta tggatgctcac 120  
aatatgtccaa gacgaagcat ggctaaaggg cttgagccaa acaagtgcgg actcttatct 180  
gggtggaaaga atgtttatga attgaattgg gattgcgaga tggaaagcaaa agctcaggaa 240  
tggggcagacg gatgtcccag ctctttccag acatttgatc caacatgggg gcagaactac 300  
gcgcacgtaca tgggatcgat tgctgatccg cttccatacg cttccatggc tggtaatggg 360  
tgggtgtcgaa aatttagaaac cgttaggactt acggatcctg ataaacaagta cactaacagt 420  
gcaatgttcc gatttgctaa tatggcaaat ggtaaagctt cagctttgg atgtgcatac 480  
gcgttgtgcg caggaaaact atccatcaat tgcatttaca acaagatagg atacatgacc 540  
aatgttatca tttatgaaaa aggagatgcc tggatcgtg acgctgaatg caccacctac 600  
tcagactcac aatgcaaaaa cggcttttc tataaggcac ctcaagctcc agtcgttgag 660  
actttcacaa tggcccttc ggtcacggac cagtcggatc aggccgcgtca aaacttcttg 720  
gacaccata acaaatttgcg tacaagcctt gccaaggggac ttggaaagctga tggaaattgcc 780  
gctggagcat ttgcaccaat gccaagcaa atgcggaaaac tggtaaaaata cagctgcaca 840  
gttgaagcaa acgcccggaaac atgggcaaaa ggtatgcctt accagcatc aacaagcgca 900  
cagagaccag gactcggtga aaatctttat atgatcagca ttaacaacat gcctaaaatt 960  
caaaccgcgg aggactcctc aaaggcttgg tggatcgtg tggaaagactt cggagtcgg 1020  
tctgacaaca ttctgaccca agcagttttt gatcgtggcg ttggacattt cacacaaatg 1080  
gcatgggaag gaactactga aattggatgt tttgtggaga attgtccaaac attcactttat 1140  
tccgtatgcc aatatggtcc agcgggaaac tacatgaacc aactaatcta taccaggc 1200  
tcaccatgca cagctgacgc cgattgccc ggaaccaga catgcgtgt cgctgaagca 1260  
ttatgtgtta tcccttagta aattttctat gcaactctt gaaagtctata ataaatatgc 1320  
aaaaattaaa aaaaaaaaaa a 1341

<210> 3

<211> 473  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Amino Acid Sequence

<400> 3  
Met Asn Val Val Leu Ser Ala Val Thr Leu Phe Leu Ile Phe Arg Tyr  
1 5 10 15  
Ala Gln Thr Val Asn Ile Glu Gly Ser Gly Gly Asn Asp Glu Leu Leu  
20 25 30  
Glu Gln Asn Val Trp Asn Asp Val Asp Asp Lys Val Val Glu Ala Leu  
35 40 45  
Gly Gly Leu Asp Asp Glu Leu Leu Thr Glu His Val Cys Asn Lys Ser  
50 55 60  
Thr Ile Thr Gln Leu Gln Gln Glu Ile Ile Leu Thr Thr His Asn Glu  
65 70 75 80  
Leu Arg Arg Ser Leu Ala Phe Gly Lys Gln Arg Asn Lys Arg Gly Leu  
85 90 95  
Met Asn Gly Ala Arg Asn Met Tyr Lys Leu Asp Trp Asp Cys Glu Leu  
100 105 110  
Ala Ser Leu Ala Ala Asn Trp Ser Thr Ser Cys Pro Gln His Phe Met  
115 120 125  
Pro Gln Ser Val Leu Gly Ser Asn Ala Gln Leu Phe Lys Arg Phe Tyr  
130 135 140  
Phe Tyr Phe Asp Gly His Asp Ser Thr Val His Met Arg Asn Ala Met  
145 150 155 160  
Lys Tyr Trp Trp Gln Gln Gly Glu Lys Gly Asn Glu Asp Gln Lys  
165 170 175  
Asn Arg Phe Tyr Ala Arg Arg Asn Tyr Phe Gly Trp Ala Asn Met Ala  
180 185 190  
Lys Gly Lys Thr Tyr Arg Val Gly Cys Ser Tyr Ile Met Cys Gly Asp  
195 200 205

Gly Glu Ser Ala Leu Phe Thr Cys Leu Tyr Asn Glu Lys Ala Gln Cys  
210 215 220

Glu Lys Glu Met Ile Tyr Glu Asn Gly Lys Pro Cys Cys Glu Asp Lys  
225 230 235 240

Asp Cys Phe Thr Tyr Pro Gly Ser Lys Cys Leu Val Pro Glu Gly Leu  
245 250 255

Cys Gln Ala Pro Ser Met Val Lys Asp Asp Gly Ser Phe Gln Cys  
260 265 270

Asp Asn Ser Leu Val Ser Asp Val Thr Arg Asn Phe Thr Leu Glu Gln  
275 280 285

His Asn Phe Tyr Arg Ser Arg Leu Ala Lys Gly Phe Glu Trp Asn Gly  
290 295 300

Glu Thr Asn Thr Ser Gln Pro Lys Ala Ser Gln Met Ile Lys Met Glu  
305 310 315 320

Tyr Asp Cys Met Leu Glu Arg Phe Ala Gln Asn Trp Ala Asn Asn Cys  
325 330 335

Val Phe Ala His Ser Ala His Tyr Glu Arg Pro Asn Gln Gly Gln Asn  
340 345 350

Leu Tyr Met Ser Ser Phe Ser Asn Pro Asp Pro Arg Ser Leu Ile His  
355 360 365

Thr Ala Val Glu Lys Trp Trp Gln Glu Leu Glu Glu Phe Gly Thr Pro  
370 375 380

Ile Asp Asn Val Leu Thr Pro Glu Leu Trp Asp Leu Lys Gly Lys Ala  
385 390 395 400

Ile Gly His Tyr Thr Gln Met Ala Trp Asp Arg Thr Tyr Arg Leu Gly  
405 410 415

Cys Gly Ile Ala Asn Cys Pro Lys Met Ser Tyr Val Val Cys His Tyr  
420 425 430

Gly Pro Ala Gly Asn Arg Lys Asn Asn Lys Ile Tyr Glu Ile Gly Asp  
435 440 445

Pro Cys Glu Val Asp Asp Asp Cys Pro Ile Gly Thr Asp Cys Glu Lys  
450 455 460

Thr Thr Ser Leu Cys Val Ile Ser Lys  
465 470

<210> 4  
<211> 1422  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:cDNA Nucleotide Sequence

<400> 4  
atgaacgtgg tccttccgc tgcactctt tttcttattt ttcgatatgc gcagactgtg 60  
aatatagaag gcagtggagg aatgtatgg cttcttgac agaacgtgtt gaacgtatgt 120  
gacgacaagg ttgttagaagc acttgggtt cttgtatgtt aactgttac acgaaatgtt 180  
tgcataatcaat caacgtatcac tcagctacag caggagatca tctgacaac ccacaatgaa 240  
ttacgaagat cattggctt cggaaagaa agaaacaaga gaggcttcat gaacgggtcg 300  
agaaatatgtt ataaactggat ttgggattgtt gaactggcat cacttgcacg caattggatca 360  
accccttgcc ctcagcactt tgcgttaccc tccgttacttgc gctccaaacgc ttagctttt 420  
aaggctttctt atttttattt tgcgttgcac gactctactg tacatatgttgc aaacgcgttgc 480  
aagtatttgcgtt ggcagcaagg tgaagaaaaa ggcaatggagg atcagaaaaa tagattctat 540  
ggccagacgaa attttttggat atggcaaaac atggcaaaag gaaaaacata tcgagttgg 600  
tgcgttata ttatgttgcggt cgcgttgcac tctgttacttgc tcaacttgc ttataacgaa 660  
aaagcccaat gcgaaaaaaga aatgatttac gaaaatggaa aaccctgttgc tgaggataaa 720  
gactgtttca cttatccagg atcaaaaatgtt ttagtacccg aaggattatgtt tcaaggcacct 780  
tctatgttacggt aggtatgttgc aggaagtttcaatgttgcacttgc ttcgttgc 840  
acccgcattt tcaacttgcgtt gcaacacaat ttttataatgttgc tctgttgc aaaaagggtttt 900  
gaatggatgtt gggaaacaaa cacttcccg cccaaaggcttgcgttgc tcaatgttgc 960  
tatgttgcgtt tgcgttgcacaa aactggcaatgttgcgtt ttttgcacac 1020  
tcggcacattt acggaaaagacc gaatcgggtt cagaatgttgc tcaacttgc ttcgttgc 1080  
cctgttgcgtt acatacggcc gtcgttgcgtt ggtggcggatgttgc 1140  
ttcggttgcgtt caattgttgcgtt cgttgcgttgc ttcgttgcgtt ggtggcggatgttgc 1200  
ataggacattt acactcggatgttgc ggcgttgcgtt cgttgcgttgc ttcgttgcgtt ggtggcggatgttgc 1260  
aactgttgcgtt acactcggatgttgc ggcgttgcgtt cgttgcgttgc ttcgttgcgtt ggtggcggatgttgc 1320  
aataaaaatctt atgaaatcggtt ggcgttgcgtt cgttgcgtt cgttgcgtt ggtggcggatgttgc 1380  
gattgttgcgtt ggcgttgcgtt cgttgcgtt cgttgcgtt ggtggcggatgttgc 1422

<210> 5  
<211> 218  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Clustal W  
Alignment of VAP-1, VAP-2, and Selected Other

Nematode VA Proteins.

<400> 5  
Met Phe Ser Pro Val Ile Val Ser Val Ile Phe Thr Ile Ala Phe Cys  
1 5 10 15  
  
Asp Ala Ser Pro Ala Arg Asp Gly Phe Gly Cys Ser Asn Ser Gly Ile  
20 25 30  
  
Thr Asp Lys Asp Arg Gln Ala Phe Leu Asp Phe His Asn Asn Ala Arg  
35 40 45  
  
Arg Arg Val Ala Lys Gly Val Glu Asp Ser Asn Ser Gly Lys Leu Asn  
50 55 60  
  
Pro Ala Lys Asn Met Tyr Lys Leu Ser Trp Asp Cys Ala Met Glu Gln  
65 70 75 80  
  
Gln Leu Gln Asp Ala Ile Gln Ser Cys Pro Ser Ala Phe Ala Gly Ile  
85 90 95  
  
Gln Gly Val Ala Gln Asn Val Met Ser Trp Ser Ser Ser Gly Gly Phe  
100 105 110  
  
Pro Asp Pro Ser Val Lys Ile Glu Gln Thr Leu Ser Gly Trp Trp Ser  
115 120 125  
  
Gly Ala Lys Lys Asn Gly Val Gly Pro Asp Asn Lys Tyr Asn Gly Gly  
130 135 140  
  
Gly Leu Phe Ala Phe Ser Asn Met Val Tyr Ser Glu Thr Thr Lys Leu  
145 150 155 160  
  
Gly Cys Ala Tyr Lys Val Cys Gly Thr Lys Leu Ala Val Ser Cys Ile  
165 170 175  
  
Tyr Asn Gly Val Gly Tyr Ile Thr Asn Gln Pro Met Trp Glu Thr Gly  
180 185 190  
  
Gln Ala Cys Lys Thr Gly Ala Asp Cys Ser Thr Tyr Lys Asn Ser Gly  
195 200 205  
  
Cys Glu Asp Gly Leu Cys Thr Lys Gly Pro  
210 215

<210> 6

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Clustal W  
Alignment of VAP-1, VAP-2, and selected other  
nematode VA Proteins.

<400> 6

Asp Val Pro Glu Thr Asn Gln Gln Cys Pro Ser Asn Thr Gly Met Thr  
1 5 10 15

Asp Ser Val Arg Asp Thr Phe Leu Val His Asn Glu Phe Arg Ser Ser  
20 25 30

Val Ala Arg Gly Leu Glu Pro Asp Ala Leu Gly Gly Asn Ala Pro Lys  
35 40 45

Ala Ala Lys Met Leu Lys Met Val Tyr Asp Cys Glu Val Glu Ala Ser  
50 55 60

Ala Ile Arg His Gly Asn Lys Cys Val Tyr Gln His Ser His Gly Glu  
65 70 75 80

Asp Arg Pro Gly Leu Gly Glu Asn Ile Tyr Lys Thr Ser Val Leu Lys  
85 90 95

Phe Asp Lys Asn Lys Ala Ala Lys Gln Ala Ser Gln Leu Trp Trp Asn  
100 105 110

Glu Leu Lys Glu Phe Gly Val Gly Pro Ser Asn Val Leu Thr Thr Ala  
115 120 125

Leu Trp Asn Arg Pro Gly Met Gln Ile Gly His Tyr Thr Gln Met Ala  
130 135 140

Trp Asp Thr Thr Tyr Lys Leu Gly Cys Ala Val Val Phe Cys Asn Asp  
145 150 155 160

Phe Thr Phe Gly Val Cys Gln Tyr Gly Pro Gly Gly Asn Tyr Met Gly  
165 170 175

His Val Ile Tyr Thr Met Gly Gln Pro Cys Ser Gln Cys Ser Pro Gly  
180 185 190

Ala Thr Cys Ser Val Thr Glu Gly Leu Cys Ser Ala Pro  
195 200 205

<210> 7  
<211> 207  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Clustal W  
Alignment of VAP-1, VAP-2, and selected other  
nematode VA proteins.

<400> 7  
Met Asn Tyr Leu Leu Leu Val Val Ala Leu Ala Val Gly Cys Ser Ala  
1 5 10 15  
  
Asp Phe Gly Ser Ser Gly Gln Asn Gly Ile Ile Asn Ala His Asn Thr  
20 25 30  
  
Leu Arg Ser Lys Ile Ala Lys Gly Thr Tyr Val Ala Lys Gly Thr Gln  
35 40 45  
  
Lys Ser Pro Gly Thr Asn Leu Leu Lys Met Lys Trp Asp Ser Ala Val  
50 55 60  
  
Ala Ala Ser Ala Gln Asn Tyr Ala Asn Gly Cys Pro Thr Gly His Ser  
65 70 75 80  
  
Gly Asp Ala Gly Leu Gly Glu Asn Leu Tyr Trp Tyr Trp Thr Ser Gly  
85 90 95  
  
Ser Leu Gly Asp Leu Asn Gln Tyr Gly Ser Ala Ala Ser Ala Ser Trp  
100 105 110  
  
Glu Lys Glu Phe Gln Asp Tyr Gly Trp Lys Ser Asn Leu Met Thr Ile  
115 120 125  
  
Asp Leu Phe Asn Thr Gly Ile Gly His Ala Thr Gln Met Ala Trp Ala  
130 135 140  
  
Lys Ser Asn Leu Ile Gly Cys Gly Val Lys Asp Cys Gly Arg Asp Ser  
145 150 155 160  
  
Asn Gly Leu Asn Lys Val Thr Val Val Cys Gln Tyr Lys Pro Gln Gly  
165 170 175  
  
Asn Phe Ile Asn Gln Tyr Ile Tyr Val Ser Gly Ala Thr Cys Ser Gly  
180 185 190

Cys Pro Ser Gly Thr Ser Cys Glu Thr Ser Thr Gly Leu Cys Val  
195 200 205

<210> 8  
<211> 231  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Clustal W  
Alignment of VAP-1, VAP-2, and selected other  
nematode VA proteins.

<400> 8  
Met Ser Asn Lys Leu Ile Ile Ser Ile Leu Ile Leu Thr Ile Ile Tyr  
1 5 10 15

Thr Val Val Asn Ser Leu Thr Val Pro Glu Gln Asn Ala Val Val Asp  
20 25 30

Cys Ile Asn Lys Tyr Arg Ser Gln Leu Ala Asn Gly Lys Thr Lys Asn  
35 40 45

Lys Asn Gly Gly Asn Phe Pro Ser Gly Lys Asp Ile Leu Glu Val Ser  
50 55 60

Tyr Ser Lys Asp Leu Glu Lys Ser Ala Gln Arg Trp Ala Asn Lys Cys  
65 70 75 80

Ile Phe Asp His Asn Gly Thr Asp Leu Tyr Ser Gly Gly Lys Phe Tyr  
85 90 95

Gly Glu Asn Leu Tyr Leu Asp Gly Asp Phe Glu His Lys Asn Ile Thr  
100 105 110

Gln Leu Met Ile Asp Ala Cys Asn Ala Trp Trp Gly Glu Ser Thr Thr  
115 120 125

Asp Gly Val Pro Pro Ser Trp Ile Asn Asn Phe Leu Pro Thr Asp Asn  
130 135 140

Lys Glu Asn Asp Glu Lys Phe Glu Ala Val Gly His Trp Thr Gln Met  
145 150 155 160

Ala Trp Ala Lys Thr Tyr Gln Ile Gly Cys Ala Leu Lys Val Cys His  
165 170 175

Lys Pro Asp Cys Asn Gly Asn Leu Ile Asp Cys Arg Tyr Tyr Pro Gly  
180 185 190

Gly Asn Gly Met Gly Ser Pro Ile Tyr Gln Gln Gly Lys Pro Ala Ser  
195 200 205

Gly Cys Gly Lys Ala Gly Pro Ser Thr Lys Tyr Ser Gly Leu Cys Lys  
210 215 220

Pro Asp Pro His Gln Asn Asn  
225 230